

SEQUENCE LISTING

<110> Eppihimer, Michael J.
 Schaub, Robert G.
 Harris, Alan

<120> Inhibition of Thrombosis by Treatment with
 P-Selectin Antagonists

<130> GFN-5398

<140>

<141>

<150> 60/193,787

<151> 2000-03-31

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1649

<212> DNA

<213> Homo sapiens

<400> 1

```

gccacttctt ctgggcccac gaggcagctg tcccctgtct tgctgagcac ggtggtgcca 60
tgctcttgca actcctcctg ttgctgatcc tactgggccc tggcaacagc ttgcagctgt 120
gggacacctg ggcagatgaa gccagagaaag ccttgggtcc cctgcttgcc cgggaccgga 180
gacaggccac cgaatatgag tacctagatt atgatttctt gccagaaacg gaggctccag 240
aaatgctgag gaacagcact gacaccactc ctctgactgg gcctggaacc cctgagteta 300
ccactgtgga gcctgctgca aggcgttcta ctggcctgga tgcaggaggg gcagtcacag 360
agctgaccac ggagctggcc aacatgggga acctgtccac ggattcagca gctatggaga 420
tacagaccac tcaaccagca gccacggagg cacagaccac tccactggca gccacagagg 480
cacagacaac tcgactgacg gccacggagg cacagaccac tccactggca gccacagagg 540
cacagaccac tccaccagca gccacggaag cacagaccac tcaaccaca ggcctggagg 600
cacagaccac tgcaccagca gccatggagg cacagaccac tgcaccagca gccatggagg 660
cacagaccac tccaccagca gccatggagg cacagaccac tcaaccaca gccatggagg 720
cacagaccac tgcaccagaa gccacggagg cacagaccac tcaaccaca gccacggagg 780
cacagaccac tccactggca gccatggagg ccctgtccac agaaccacgt gccacagagg 840
ccctgtccat ggaacctact accaaaagag gtctgttcat acccttttct gtgtcctctg 900
ttactcaciaa gggcattccc atggcagcca gcaattgtgc cgtcaactac ccagtggggg 960
ccccagacca catctctgtg aagcagtgcc tgctggccat cctaactctg gcgctgggtg 1020

```

ccactatctt cttcgtgtgc actgtggtgc tggcgggtccg cctctcccgc aagggccaca 1080
 tgtaccccggt gcgtaattac tccccaccg agatgggtctg catctcatcc ctgttgccgt 1140
 atgggggtga ggggccctct gccacagcca atgggggct gtccaaggcc aagagcccg 1200
 gcctgacgcc agagcccagg gaggaccgtg agggggatga cctcaccctg cacagcttcc 1260
 tcccttagct cactctgcca tctgttttg caagacccca cctccacggg ctctcctggg 1320
 ccacccctga gtgccagac ccacatccac agctctgggc ttctcggag acccctgggg 1380
 atggggatct tcaggggaag aactctgggc acccaaacag gacaagagca gcctggggcc 1440
 aagcagacgg gcaagtggag ccacctcttt cctccctccg cggatgaagc ccagccacat 1500
 ttacgccgag gtccaaggca ggaggccatt tacttgagac agattctctc ctttttctgc 1560
 tcccccatct tctctgggc cctctaacat ctcccatggc tctcccgct tctcctggtc 1620
 actggagtct cctcccatg tacccaagg 1649

<210> 2
 <211> 402
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
 1 5 10 15
 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
 20 25 30
 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
 35 40 45
 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
 50 55 60
 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 65 70 75 80
 Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
 85 90 95
 Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
 100 105 110
 Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
 115 120 125
 Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr
 130 135 140
 Arg Leu Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu
 145 150 155 160
 Ala Gln Thr Thr Pro Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro
 165 170 175

Thr Gly Leu Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala Gln
 180 185 190
 Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Pro Pro Ala Ala
 195 200 205
 Met Glu Ala Gln Thr Thr Gln Thr Thr Ala Met Glu Ala Gln Thr Thr
 210 215 220
 Ala Pro Glu Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu
 225 230 235 240
 Ala Gln Thr Thr Thr Leu Ala Ala Met Glu Ala Leu Ser Thr Glu Pro
 245 250 255
 Ser Ala Thr Glu Ala Leu Ser Met Glu Pro Thr Thr Lys Arg Gly Leu
 260 265 270
 Phe Ile Pro Phe Ser Val Ser Ser Val Thr His Lys Gly Ile Pro Met
 275 280 285
 Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
 290 295 300
 Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
 305 310 315 320
 Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
 325 330 335
 Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
 340 345 350
 Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
 355 360 365
 Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
 370 375 380
 Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu Thr Leu His Ser Phe
 385 390 395 400
 Leu Pro

<210> 3
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(939)

<400> 3
 atg cct ctg caa ctc ctc ctg ttg ctg atc cta ctg ggc cct ggc aac 48
 Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
 1 5 10 15

agc ttg cag ctg tgg gac acc tgg gca gat gaa gcc gag aaa gcc ttg 96
 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
 20 25 30

ggt ccc ctg ctt gcc cgg gac cgg aga cag gcc acc gaa tat gag tac 144
 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
 35 40 45

cta gat tat gat ttc ctg cca gaa acg gag cct cca gaa atg ctg agg 192
 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
 50 55 60

aac agc act gac acc act cct ctg act ggg cct gga acc cct gag tct 240
 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 65 70 75 80

acc act gtg gag cct gct gcg cgg ccg cac aca tgc cca ccg tgc cca 288
 Thr Thr Val Glu Pro Ala Ala Arg Pro His Thr Cys Pro Pro Cys Pro
 85 90 95

gca cct gaa gcc ctg ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa 336
 Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
 100 105 110

ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg 384
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 115 120 125

gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac 432
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 130 135 140

gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag 480
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 145 150 155 160

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac 528
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 165 170 175

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 576
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 180 185 190

gcc ctc cca gtc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag 624
 Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 195 200 205

ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg 672
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 210 215 220

acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc 720
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 225 230 235 240

agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac 768
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 245 250 255

tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc 816

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 260 265 270
 tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc 864
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 275 280 285
 ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag 912
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 290 295 300
 aag agc ctc tcc ctg tcc ccg ggt aaa tga 942
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 305 310
 <210> 4
 <211> 313
 <212> PRT
 <213> Homo sapiens
 <400> 4
 Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
 1 5 10 15
 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
 20 25 30
 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
 35 40 45
 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
 50 55 60
 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 65 70 75 80
 Thr Thr Val Glu Pro Ala Ala Arg Pro His Thr Cys Pro Pro Cys Pro
 85 90 95
 Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
 100 105 110
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 115 120 125
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 130 135 140
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 145 150 155 160
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 165 170 175
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 180 185 190
 Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
305 310

[illegible]